

Use Case: 1              Browse CGAP Web Site

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CHARACTERISTIC INFORMATION

**Goal in Context:** To find genetic information about the molecular characterization of normal, precancerous, and malignant cells, utilizing the tools available at the CGAP site.

**Preconditions:** The Users browser has been directed to the web site URL.

**Success End Condition:** The user finds genetic information of interest.

**Failed End Condition:** The user is unable to use the web site to find information

**Primary Actor:** Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with a screen in which they can:
  - a. View gene information, they can:
    - Find genes by tissue, function, cytogenetic location, title (use case [Find Genes by Attribute](#))
    - Find genes by symbol, accession number, cluster number (use case [Find Genes by Handle](#))
    - Find genes by search by nucleotide sequences (use case [Find Genes by Sequence](#))
    - Lists of candidate, validated, and confirmed SNPs in genes (use case [Browse CGAP Genetic Annotation Initiative Site](#))
    - View the curated lists of cancer genes (use case [View Curated Lists](#))
  - b. View chromosome information
    - View Mitelman Database of Chromosome Aberrations in Cancer Database (use case [Browse Mitelman Database](#))
    - Cancer Chromosome Aberration Project (CCAP) (use case [Browse CCAP](#))
    - Cytogenetic position of FISH-mapped BAC Clones (use case [Find CCAP Clones](#))
    - Recurrent chromosome aberrations in cancer (use case [Find Chromosome Aberrations](#))
    - Genetic and physical map positions of SNPs (use case [Browse SNP Maps](#))
    - Physical map position of genes (use case [Link to External Site](#))
  - c. View tissue information
    - Browse the collection of tissue-specific libraries (use case [Browse Libraries](#))
    - Examine patterns of gene transcript expression across tissues and libraries (use case [Summarize Libraries](#))
    - Analyze gene expression (present/not present) using the Library Xprofiler (use case [Analyze Expression with Library XProfiler](#))
    - Analyze gene expression (more expressed/less expressed) using the Gene Expression Spreadsheet (use case [Create Gene Expression Spread Sheet](#))
    - Analyze CGAP Serial Analysis of Gene Expression (SAGE) (use case [SAGE Analysis](#))
    - Find SNPs in genes expressed in a given tissue (use case [Browse Expression-Based SNP Imagemaps](#))
2. The user may select to continue to any part of CCGAP.

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EXTENSIONS

- 2a. The user is unable to find the item in CGAP they are interested in.

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Superordinate Use Case:

Subordinate Use Cases

[Find Genes by Attribute](#)  
[Find Genes by Handle](#)  
[Find Genes by Sequence](#)  
[Browse CGAP Genetic Annotation Initiative Site](#)  
[View Curated Lists](#)  
[Browse Mitelman Database](#)  
[Browse CCAP](#)  
[Find CCAP Clones](#)  
[Find Chromosome Aberrations](#)  
[Browse SNP Maps](#)  
[Link to External Site](#)  
[Browse Libraries](#)  
[Summarize Libraries](#)  
[Analyze Expression with Library XProfiler](#)  
[Create Gene Expression Spread Sheet](#)  
[Browse Expression-Based SNP Imagemaps](#)

Use Case: 2                      Browse Libraries

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CHARACTERISTIC INFORMATION

Goal in Context: A researcher wishes to find out more about the tissue libraries indexed at the CGAP site.

Preconditions: The user has selected the tissue tab from the CGAP site.

Success End Condition: The user has found libraries of interest.

Failed End Condition: The user is unable to find libraries.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO:

1. The user selects Browse Libraries from the site
2. The user may select to limit the libraries returned by:
  - a. Organism
  - b. Scope (project the library comes from)
  - c. Library Type (protocol for biological source)
  - d. Library Protocol
  - e. Library Title
  - f. Tissue
  - g. Histology
3. The user may select to order the results of the search
4. The user submits the search
5. The user is presented with a list of libraries that match the search criteria (use case View Library List ).

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EXTENSIONS

- 5a. There are no matching libraries
- 5a1. The user enters new search criteria

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Superordinate Use Case:

Browse CGAP Web Site

Subordinate Use Cases:

Link to External Site

Use Case: 3                      Summarize Libraries

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to compare the library to gene relationships.

Preconditions: The user has selected the tissue tab from the CGAP site.

Success End Condition: The user finds information relating libraries to the genes within them.

Failed End Condition: The user is unable to find libraries and gene information of interest.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user selects Summarize Libraries from the site
2. The user may select to limit the libraries returned by:
  - a. Organism
  - b. Scope (project the library comes from)
  - c. Library Type (protocol for biological source)
  - d. Library Protocol
  - e. Library Title
  - f. Tissue
  - g. Histology
3. The user may select to summarize the list by:
  - a. Tissue
  - b. Title
  - c. Type
  - d. Histology
  - e. Protocol
4. The user submits the search
5. The user is presented with libraries, which have been summarized by the selected criteria, as well as the combined set of libraries. The list includes.
  - a. Subset (the summarization item)
  - b. Libraries
  - c. Sequences (number of)
  - d. Unique Genes - Genes that are uniquely expressed in a given tissue type  
Known - entry in NCBI's LocusLink database  
Unknown - no entry in NCBI's LocusLink database
  - e. Nonunique Genes - Genes that are also expressed in other tissue types (known and unknown)  
Known - entry in NCBI's LocusLink database  
Unknown - no entry in NCBI's LocusLink databaseAs columns.
6. The user may select to view the Libraries (use case View Library List)
7. The user may select to view any of the Genes (use case View Gene List)

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EXTENSIONS

- 5a. There are no matching libraries
  - 5a1. The user enters new search criteria

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SUB-VARIATIONS

RELATED INFORMATION (optional)

Superordinate Use Case:

Browse CGAP Web Site

Subordinate Use Cases:

View Library List

View Gene List

Use Case: 4                      Analyze Expression with Library XProfiler

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to compare the expression of genes for 2 sets of libraries, based on the input criteria for each set.

Preconditions: The user has selected the tissue tab from the CGAP site

Success End Condition: The user finds information relating the sets of libraries and the expression of the genes within them.

Failed End Condition: The user is unable to find libraries and gene expression information of interest

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user selects Library Expression Profiler from the site
2. The user is presented with a screen in which they may select to limit both the libraries returned by:
  - a. Organism
  - b. Scope (project the library comes from)
  - c. Minimum Sequences
3. The user can also restrict the individual sets of libraries by:
  - a. Library Type (protocol for biological source)
  - b. Library Protocol
  - c. Library Title
  - d. Tissue (either to include or exclude)
  - e. Histology
4. The user may select to order the list by:
  - a. Tissue
  - b. Title
  - c. Type
  - d. Histology
  - e. Protocol
5. The user submits the search
6. The user is presented with a listing of all libraries fulfilling each set of search criteria, the list includes
  - a. Library Name
  - b. Total Sequences
  - c. Key Words
7. The user may select to include or exclude a given library from the final search result.
8. The user may drill down to library info (use case [View Library List](#) step 2).
9. The user submits the search
10. The user is presented with number libraries included with each set, there is also a list that has been summarized by the library set selection. The list includes.
  - a. Unique Genes - Genes that are uniquely expressed in a given tissue type  
Known - entry in NCBI's LocusLink database  
Unknown - no entry in NCBI's LocusLink database
  - b. Nonunique Genes - Genes that are also expressed in other tissue types (known and unknown)  
Known - entry in NCBI's LocusLink database  
Unknown - no entry in NCBI's LocusLink databaseAs columns, summarized by
  - a. First Set Only
  - b. Second Set Only
  - c. First and Second Set
  - d. First or Second Set
  - e. First minus Second Set
  - f. Second minus First Set
11. The user may select to view the Libraries (use case [View Library List](#))
12. The user may select to view any of the Genes (use case [View Gene List](#))

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EXTENSIONS

- 5a. There are no matching libraries
  - 5a1. The user enters new search criteria

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Superordinate Use Case:

[Browse CGAP Web Site](#)

Subordinate Use Cases:

[View Library List](#)

[View Gene List](#)

Use Case: 5                      Analyze Expression with Gene Expression Spreadsheet

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to compare the expression of genes for 2 sets of libraries, based on the input criteria for each set.

Preconditions: The user has selected the tissue tab from the CGAP site

Success End Condition: The user finds information relating the sets of libraries and the expression of the genes within them.

Failed End Condition: The user is unable to find libraries and gene expression information of interest.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user selects Gene Expression Spreadsheet from the site
2. The user is presented with a screen in which they may select to limit both the libraries returned by:
  - a. Organism
  - b. Scope (project the library comes from)
  - c. Minimum Sequences
3. The user can also restrict the individual sets of libraries by:
  - a. Library Type (protocol for biological source)
  - b. Library Protocol
  - c. Library Title
  - d. Tissue (either to include or exclude)
  - e. Histology
4. The user may select to order the list by:
  - a. Tissue
  - b. Title
  - c. Type
  - d. Histology
  - e. Protocol
5. The user submits the search
6. The user is presented with a listing of all libraries fulfilling each set of search criteria, the list includes
  - a. Library Name
  - b. Total Sequences
  - c. Key Words
7. The user may select to include or exclude a given library from the final search result.
8. The user may select to set a minimum number of sequences for the target.
9. The user may drill down to library info (use case [View Libraries List](#) step 2).
10. The user submits the search
11. The user is presented with the gene expression spreadsheet results. The results include:
  - a. The total sequences in the first set
  - b. The total sequences in the second set
  - c. The total libraries in the first set
  - d. The total libraries in the second set
  - e. A list of all genes which match the search criteria, the list includes
    - The gene symbol
    - Link to gene information
    - Number of libraries in the first set the gene is found in
    - Number of libraries in the second set the gene is found in
    - Number of sequences in the first set the gene is found in
    - Number of sequences in the second set the gene is found in
    - The sequence odds, first to second set
    - Fisher?
12. The user may select to view the Libraries (use case [View Library List](#))
13. The user may select to view any of the Genes (use case [View Gene Information](#))
14. The user may download a tab delimited version of the results (use case [Download Data](#))

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EXTENSIONS

- 5a. There are no matching libraries  
5a1. The user enters new search criteria

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Superordinate Use Case:

[Browse CGAP Web Site](#)

Subordinate Use Cases:

[View Library List](#)

[View Gene Information](#)

Use Case: 6              View Library List

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to browse a list of libraries

Preconditions: The user has browsed CGAP site to the point where they are presented with the Library List.

Success End Condition: The user finds information about the libraries.

Failed End Condition: The user is unable to find information about the libraries

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The list includes:
  - a. Title
  - b. Tissue
  - c. Histology
  - d. Type
  - e. Protocol
  - f. KeywordsAs columns.
2. The user may select a library to see the details of it.
3. If available, the user may select to see the Unigene details of the library, the user is redirected to the Unigene site, in a new window (use case Link to External Site).
4. If available, the user may select to see other libraries of the same tissue, this repeats the use case at step 1.

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EXTENSIONS

- 5a. There are no matching libraries
  - 5a1. The user enters new search criteria

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Superordinate Use Case:

Browse Tissue Libraries

Summarize Libraries

Analyze Expression with Library XProfiler

Subordinate Use Cases:

View Library List

View Gene List

Use Case: 7                      SAGE Analysis

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes view CGAP data utilizing the SAGE tools.

Preconditions: The user has selected the tissue tab from the CGAP site.

Success End Condition: The user connects to the proper SAGE tool.

Failed End Condition: The user is unable to connect to the SAGE tool.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1.    The user is presented with a list of SAGE tools which have CGAP data, these include:
  - a.        The Library Cross-Profiler
  - b.        The Virtual Northern Blots Tool
2.    The user may select to go to the tool site (use case [Link to External Site](#)).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Superordinate Use Case:

Subordinate Use Cases:

[Link to External Site](#)

Use Case: 8                      Browse Mitelman Database

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to use CGAP to find information that is stored in the Mitelman Database of Chromosome Aberrations in Cancer..

Preconditions: The user has selected the Mitelman Database from the chromosome tab at the CGAP site.

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with ways to search the Mitelman Database, these include:
  - a. Search the database with case information by short (use case Search Mitelman Cases by Short Form) and long form (use case Search Mitelman Cases by Long Form)
  - b. Search database of molecular biology and clinical associations (use case Search Mitelman Associations)
  - c. Search all Mitelman databases by author, journal, year (use case Search Mitelman by Journal Information)
2. The user may select to perform any search.

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Superordinate Use Case:

Browse CGAP Web Site

Subordinate Use Cases:

Search Mitelman Cases by Short Form

Search Mitelman Cases by Long Form

Search Mitelman Associations

Search Mitelman by Journal Information



Use Case: 9                      Search Mitelman Cases by Short Form

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to use CGAP to find information that is stored in the Mitelman Case Database utilizing the short form.

Preconditions: The user has selected the Mitelman Database from the chromosome tab at the CGAP site and proceeded to the short form search

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1.    The user is presented with fields to restrict the search, these include:
  - a.      Abnormality – the abnormal element of a karyotype, including if it is the only one
  - b.      Breakpoint – the cytogenetic band location of abnormality
  - c.      Topography – Tumor site
  - d.      Morphology – Tumor histology
  - e.      Special Morphology – Rare tumor types
2.    The user may use logical AND/OR with Abnormality and Breakpoint.
3.    The user submits the search.
4.    Use case View Chromosome Aberration Case List is performed

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Superordinate Use Case:

Browse Mitelman Database

Subordinate Use Cases:

View Chromosome Aberration Case List

Use Case: 10            View Chromosome Aberration Case List

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher is browsing a Mitelman Case List.

Preconditions: The user has used the Mitelman Case Database to find a list of cases.

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with a list of journal articles (Chromosome Aberration Case List) , with links to article information, matching the search criteria, the list includes the following information on the cases in the article:
  - a. Link to Case Information
  - b. Case Number
  - c. Morphology
  - d. Topography
  - e. Abnormality
2. The user may select to view the article information (use case View Article Information).
3. The user may select to view the article information (use case View Case Information).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Search Mitelman Cases by Short Form

Search Mitelman Cases by Long Form

Subordinate Use Cases:

View Article Information

View Case Information

Use Case: 11            View Article List.

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#### CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher is browsing a Mitelman Article List.

Preconditions: The user has used the Mitelman Case Database to find a list of articles.

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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#### MAIN SUCCESS SCENARIO

1. The user is presented with a list of journal articles (Reference List), with links to article information, matching the search criteria.
2. The user may select to view the article information (use case View Article Information).

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#### EXTENSIONS

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#### SUB-VARIATIONS

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#### RELATED INFORMATION (optional)

Superordinate Use Case:

View Article Information

Subordinate Use Cases:

View Article Information

Use Case: 12            View Article Information

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher is viewing information on an article in the Mitelman Database.

Preconditions: The user has used the Mitelman Case Database to find an article.

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1.    The user is presented with information pertaining to an article in the Mitelman Database, this includes:
  - a.    Reference Number
  - b.    Title
  - c.    Authors
  - d.    Journal
  - e.    Volume
  - f.    Year
2.    The user may select an author to view the authors' articles (use case View Article List).
3.    The user may select the journal to view articles in the journal (use case View Article List).
4.    The user may select the PubMed link to view PubMed information (use case Link to External Site).
5.    The user may select to browse all cases in the article (use case View Chromosome Aberration Case List).
6.    The user may select to view molecular biologic associations with the article (use case View Biologic Associations).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Search Mitelman Cases by Short Form

Search Mitelman Cases by Long Form

Subordinate Use Cases:

View Article List

Search Mitelman by Journal Information

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher is viewing information on a case in the Mitelman Database.

Preconditions: The user has used the Mitelman Case Database to find a case.

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1.    The user is presented with information pertaining to an case in the Mitelman Database, this includes:
  - a.    Reference to Article Case Found In
  - b.    Sex
  - c.    Age
  - d.    Race
  - e.    Country
  - f.    Series
  - g.    Hereditary Disorder
  - h.    Present Tumor
    - Topography
    - Immunophenotype
    - Morphology
    - Tissue
  - i.    Previous Tumor
    - Topography
    - Morphology
    - Treatment
2.    The user may select to view the article the case came from (use case View Article Information)

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

    Search Mitelman Cases by Short Form

    Search Mitelman Cases by Long Form

Subordinate Use Cases:

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to use CGAP to find information that is stored in the Mitelman Case Database utilizing the long form.

Preconditions: The user has selected the Mitelman Database from the chromosome tab at the CGAP site and proceeded to the long form search

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with fields to restrict the search, these include:
  - a. Cytogenetic Characteristics
    - Abnormality – the abnormal element of a karyotype, including if it is the only one
    - Breakpoint – the cytogenetic band location of abnormality
    - Number of Clones
    - Number of Chromosomes
  - b. Patient Characteristics
    - Sex
    - Age
    - Race
    - Country
    - Series
    - Hereditary Disorder
    - Special Hereditary Disorder
  - c. Present Tumor
    - Topography
    - Immunophenotype
    - Morphology
    - Special Morphology
    - Tissue
  - d. Previous Tumor
    - Exists
    - Topography
    - Morphology
    - Treatment
  - e. Reference
    - Authors
    - Journal
    - Year
    - Specific ID Number (Ref Number, Case Number, Investigation Number)
2. The user may use logical AND/OR with Abnormality and Breakpoint.
3. The user submits the search.
4. Use case View Chromosome Aberration Case List is performed

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Browse Mitelman Database

Subordinate Use Cases:

Search Mitelman Cases by Short Form

Search Mitelman Cases by Long Form

Search Mitelman Associations

Search Mitelman by Journal Information

Use Case: 15              Search Mitelman Associations

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to use CGAP to find information that is stored in the Mitelman Associations Database.

Preconditions: The user has selected the Mitelman Database from the chromosome tab at the CGAP site and proceeded to the associations

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with fields to restrict the search, these include:
  - a. Molecular Biology or Clinical Association
  - b. Abnormality – the abnormal element of a karyotype, including if it is the only one
  - c. Breakpoint – the cytogenetic band location of abnormality
  - d. Topography – Tumor site
  - e. Morphology – Tumor histology
  - f. Special Morphology – Rare tumor types
  - g. Authors
  - h. Journal
  - i. Year
  - j. Specific ID Number (Ref Number, Inv Number)
2. The user may use logical AND/OR with Abnormality and Breakpoint.
3. The user submits the search.
1. The user is presented with a list of journal articles (Association List) , with links to article information, matching the search criteria, the list includes the following information on the associations in the article:
  - a. Link to Case Information
  - b. Article Number
  - c. Morphology
  - d. Topography
  - e. Abnormality
  - f. gene designation (Molecular Biology)
2. The user may select to view the article information (use case View Article Information).
4. The user may select to view the gene information (Molecular Biology) (use case View Gene Information).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Browse Mitelman Database

Subordinate Use Cases:

View Article Information

View Gene Information

Use Case: 16              Search Mitelman by Journal Information

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to use CGAP to find information that is stored in the Mitelman Database by journal information.

Preconditions: The user has selected the Mitelman Database from the chromosome tab at the CGAP site and proceeded to the journal search.

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with fields to restrict the search, these include:

- a. Operator (Cytogenetics, Molecular Biology, Clinical Association)
  - b. Authors
  - c. Journal
  - d. Year
  - e. Reference Number
2. The user submits the search.
3. Use case View Article List is performed

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)  
Priority:  
Frequency:  
Superordinate Use Case:  
    Browse Mitelman Database  
Subordinate Use Cases:  
    View Article List



Use Case: 17            Browse CCAP Site

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to use CGAP to utilize the tools within the Cancer Chromosome Aberration Project (CCAP).

Preconditions: The user has selected the Cancer Chromosome Aberration Project from the chromosome tab at the CGAP site

Success End Condition: The user finds information in the Cancer Chromosome Aberration Project.

Failed End Condition: The user is unable find information in the Cancer Chromosome Aberration Project.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with the tools of the CCAP site, these include:
  - a. CCAP Clone Maps, an interface to access the bacterial artificial chromosome (BAC) human chromosome mapping data (use case Browse CCAP Clone Maps).
  - b. Recurrent Aberration Data, an interface to search the recurrent aberrations that were derived from the Mitelman Database of Chromosome Aberrations in Cancer (use case Search Recurrent Aberration Data).
2. The user may select to use the tools.

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Subordinate Use Cases:

    Browse CCAP Clone Maps

    Search Recurrent Aberration Data

Use Case: 18              Browse CCAP Clone Maps

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to access the bacterial artificial chromosome (BAC) human chromosome mapping data.

Preconditions: The user has selected the cytogenetic position of FISH-mapped BAC Clones from the chromosome tab at the CGAP site or the CCAP Clone Maps from the CCAP use case.

Success End Condition: The user finds information in the CCAP Clone Maps.

Failed End Condition: The user is unable to find information in the CCAP Clone Maps.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with a list of chromosome pairs. For the ones that contain clones, hyperlinks exist.
2. The user selects a hyperlinked chromosome.
3. The user is presented with a map of the chromosome, entities mapped include:
  - a. Reference idiogram, provides a spatial reference for the additional letter designations on top of the traditional G-stain 850-band nomenclature system.
  - b. Map coordinate, indicates the FISH location of the BAC clone by indicating a band or range of bands. These are linked to human neoplasm recurrent chromosomal aberration data (use case View Aberration List).
  - c. STS ID, gives the sequence tag site identifier. These are linked to additional STS mapping information (use case [Link to External Site](#)).
  - d. BAC clone ID, gives the bacterial artificial chromosome id used to order clones from Research Genetics (use case [Link to External Site](#)).
4. The user may select any of the hyperlinks for additional information.

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

[Browse CCAP Site](#)

Subordinate Use Cases:

[Link to External Site](#)

Use Case: 19              Search Recurrent Aberration Data

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#### CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to access the information that is stored in the Recurrent Chromosome Aberrations in Cancer Database.

Preconditions: The user has selected the Recurrent chromosome aberrations in cancer from the chromosome tab at the CGAP site or the Recurrent Aberration Data from the CCAP use case.

Success End Condition: The user finds information in the Recurrent Chromosome Aberrations in Cancer Database..

Failed End Condition: The user is unable to find information in the Recurrent Chromosome Aberrations in Cancer Database..

Primary Actor: Researcher

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#### MAIN SUCCESS SCENARIO

1. The user is presented with fields to restrict the search, these include:
  - a. Chromosome
  - b. Arm
  - c. Band
  - d. Aberration type
  - e. Site
  - f. Morphology
  - g. Gene
2. The user is presented a list of balanced and unbalanced chromosomal abnormalities (use case View Abnormality List)

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#### EXTENSIONS

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#### SUB-VARIATIONS

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#### RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Browse CCAP Site

Subordinate Use Cases:

View Abnormality List

Use Case: 20            View Abnormality List

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher is browsing a Mitelman Case List.

Preconditions: The user has used the Mitelman Case Database to find a list of cases.

Success End Condition: The user finds information in the Mitelman Database.

Failed End Condition: The user is unable to find information in the Mitelman Database.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with a list of balanced and unbalanced chromosomal abnormalities the list includes:
  - a. Band
  - b. Abnormality
  - c. Morphology
  - d. Site
  - e. Cases
  - f. Genes
2. The user may select to view the band information from the OMIN Database (use case Link to External Site).
3. The user may select to view a list of abnormalities having the same morphology (use case View Abnormality List).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Search Recurrent Aberration Data

View Abnormality List

Subordinate Use Cases:

Link to External Site

View Abnormality List

Use Case: 21              Browse SNP Maps

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the user is browsing the SNP information available based on position within the chromosomes.

Preconditions: The user has selected the genetic and physical map positions of SNPs from the chromosome tab of the CGAP site.

Success End Condition: The user finds information SNP information.

Failed End Condition: The user is unable to find SNP information.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1.    The user is presented with a table showing the chromosome pairs.
2.    The user may select to view the SNP Map of the chromosome.
3.    The user may select to view the Linkage Map of the chromosome.

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Browse CGAP Web Site

Subordinate Use Cases:

Use Case: 22              Find Genes by Attribute

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the user is finding genes by Find genes by tissue, function, cytogenetic location or title.

Preconditions: The user has selected to find genes by attribute from the gene tab of the CGAP site.

Success End Condition: The user finds information gene information.

Failed End Condition: The user is unable to find gene information.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is with a query screen in which they can limit the results of a search, the results can be limited by:
  - a. Organism
  - b. Title Keyword
  - c. Curated List
  - d. Pathway
  - e. Tissue
  - f. Cytogenetic Location
2. The user submits the search.
3. The user is presented with a list of genes matching the search criteria (use case View Gene List ).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Browse CGAP Web Site

Subordinate Use Cases:

View Gene List

Use Case: 23              Gene List

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to browse a list of genes.

Preconditions: The user has browsed CGAP site to the point where they are presented with the Gene List.

Success End Condition: The user finds information about the genes.

Failed End Condition: The user is unable to find information about the genes

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with a list of genes matching the search criteria, the list includes:
  1. Symbol
  2. Title
  3. Sequence
  4. Link to CGAP Gene Info
2. The user may select to view the gene information (use case View Gene Information).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Find Genes by Handle

Find Genes by Attribute

Subordinate Use Cases:

View Gene Information

Use Case: 24          View Gene Information

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the researcher wishes to view available information on a given gene.

Preconditions: The user has browsed CGAP site to the point where they are presented with a CGAP Gene Information Link.

Success End Condition: The user finds information about the genes.

Failed End Condition: The user is unable to find information about the genes

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with the following gene information:
  - a. Organism
  - b. Symbol
  - c. Title
  - d. Sequence
  - e. Database Links
    - UniGene (use case [Link to External Site](#))
    - LocusLink (use case [Link to External Site](#))
    - Libraries (use case [View Library List](#))
    - Assembly (use case [View Assembly List](#))
    - SNPs (use case [SNP List](#)) (use case [Link to External Site](#))
  - f. Cytogenetic location (from Unigene)
  - g. Link to Mitelman Database (use case [View Chromosome Aberration Case List](#))
  - h. Protein Similarity List
    - Organism
    - Protein ID (use case [Link to External Site](#))
    - % Similarity
    - Aligned aa
  - i. Computed Mus musculus orthologs (from HomoloGene)
    - Symbol
    - Title
    - Sequence
    - Link to Gene Info (use case [View Gene Information](#))
    - % Similarity
  - j. Sequence-verified clones in cluster
    - Image Clone Id
    - GenBank Accession (use case [Link to External Site](#))
2. The user may select any of the links to perform the given use cases.

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

[Gene List](#)

Subordinate Use Cases:

[Link to External Site](#)

[View Gene Information](#)

[View Library List](#)

[View Assembly List](#)

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Use Case: 25          Find Genes by Handle

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the user is finding genes by symbol, accession number or cluster number.

Preconditions: The user has selected to find genes by handle from the gene tab of the CGAP site.

Success End Condition: The user finds information gene information.

Failed End Condition: The user is unable to find gene information.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is with a query screen in which they can limit the results of a search, the results can be limited by:
  - a. Organism
  - b. Symbol, GenBank accession, or UniGene cluster id



2. The user submits the search.
3. The user is presented with a list of genes matching the search criteria (use case View Gene List).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Browse CGAP Web Site

Subordinate Use Cases:

View Gene List

Use Case: 26              Find Genes by Sequence

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the user is finding genes by nucleotide sequences.

Preconditions: The user has selected to find genes by nucleotide sequences from the gene tab of the CGAP site.

Success End Condition: The user finds information gene information.

Failed End Condition: The user is unable to find gene information.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with a new window in which they can limit the results returned by the search, they may add:
  - a. Organism
  - b. Expect, the precision of the match
  - c. Show, how many sequences to show
  - d. Sequence, sequence to search on
2. The user submits the search.
3. The user is presented with a list of sequences matching the BLAST search criteria, the list includes:
  - a. Link to GenBank Accession (use case [Link to External Site](#))
  - b. Expect
  - c. Symbol
  - d. Title
  - e. Link to CGAP Gene Info (use case [View Gene Information](#))
4. The user can select the links.

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

[Browse CGAP Web Site](#)

Subordinate Use Cases:

[Link to External Site](#)

[View Gene Information](#)

Use Case: 27              Browse CGAP Genetic Annotation Initiative Site

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the user is looking for the variants located on genes.

Preconditions: The user has selected SNP's gene tab of the CGAP site.

Success End Condition: The user finds information gene variant information.

Failed End Condition: The user is unable to find gene variant information.

Primary Actor: Researcher

-----  
MAIN SUCCESS SCENARIO

1. The user is presented with a new window in which they can:
  - a. Use CGAP-GAI Identified Variation in Genes to:
    - Find locations of SNPs in genetic and physical maps (use case Browse SNP Maps)
    - Search Candidate SNPs by gene name, gene symbol, or GenBank accession number (use case Search Candidate SNP's)
    - Search SNPs onto human reference sequences, with CDS changes Database (use case Search Protein Changes Database)
    - Candidate, Validated, and Confirmed SNP lists
  - b. SNP Finder For analyzing user-submitted trace data

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Subordinate Use Cases:

Browse SNP Maps

Search Candidate SNP's

Search Protein Changes Database

Use Case: 28              Browse SNP Maps

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the user is looking for the distribution of variants located on genes via physical and genetic maps.

Preconditions: The user has selected SNP's gene tab of the CGAP site.

Success End Condition: The user finds information gene variant information.

Failed End Condition: The user is unable to find gene variant information.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with a table showing the available chromosomes, the user can:
  - a. Select to view the SNP map of the chromosome (use case View SNP Map is performed).
  - b. Select to view the Linkage map of the chromosome (use case View Linkage Map is performed).
2. The user may select CGAP SNP Index (use case Search SNP Index is performed).
3. The user may select Cytogenetic Search (use case Search SNP's by Cytogenetic Location is performed).
4. The user may select RH Map Search (use case Search SNP's by Map Location is performed).
5. The user may select Summary Files (use case Browse SNP Summaries is performed).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Browse CGAP Genetic Annotation Initiative Site

Subordinate Use Cases:

View SNP Map

View Linkage Map

Search SNP Index

Search SNP's by Cytogenetic Location

Search SNP's by Map Location

Browse SNP Summaries

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CHARACTERISTIC INFORMATION

Goal in Context: In this use case the user is looking for the distribution of variants located on genes via physical and genetic map.

Preconditions: The user has selected SNP Map from the Browse SNP's use case.

Success End Condition: The user finds information gene variant information.

Failed End Condition: The user is unable to find gene variant information.

Primary Actor: Researcher

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MAIN SUCCESS SCENARIO

1. The user is presented with a diagram which displays:
  - a. Distribution of SNPs
    - Validated
    - Confirmed
    - Candidate
  - b. Genetic Map
  - c. Reference Markers
  - d. Physical Map
  - e. Idiogram
2. The user can select to view the distribution of SNPs for a given interval (use case Browse SNP Index)
3. The user can select to view the reference marker information (use case Search Markers)
4. The user can select to view the physical map for a given interval (use case Browse Physical Map).
5. The user can select to view the SNPs for a given cytogenetic location (use case Search SNP's by Cytogenetic Location).
6. The user can select to view the SNP map for a different chromosome (use case View SNP Map is performed).
7. The user can select to view the genes expressed for a given tissue (use case View SNP Map is performed).

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EXTENSIONS

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SUB-VARIATIONS

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RELATED INFORMATION (optional)

Priority:

Frequency:

Superordinate Use Case:

Browse SNP Maps

Subordinate Use Cases:

Browse SNP Index

Search Markers

Browse Physical Map

View SNP Map